UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/585,842	07/12/2006	Anthony Cox	2713-1-044PCT/US	7872

23565 7590 10/26/2010

KLAUBER & JACKSON
411 HACKENSACK AVENUE
HACKENSACK, NJ 07601

EXAMINER	
ZHAO, YU	

ART UNIT	PAPER NUMBER
2169	

MAIL DATE	DELIVERY MODE
10/26/2010	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/585,842	COX, ANTHONY	
	Examiner	Art Unit	
	YU ZHAO	2169	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *16 August 2010*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *25 and 29-57* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *25 and 29-57* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Continued Examination Under 37 CFR 1.114

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on **August 16, 2010** has been entered.

Response to Amendment

2. Acknowledgment is made of applicant's amendment filed on **August 16, 2010**.

Claims 25, 29-57 are presented for examination.

Claims 1-24 and 26-28 were cancelled per applicant's request.

Claims 25, 29, 33 and 54 are amended.

Response to Argument

3. Applicant's arguments filed in the amendment filed on **August 16, 2010**, have been fully considered but they are not deemed persuasive:

Examiner has re-mapped the references to the newly added limitations.

Claim Objections

4. **Claims 25 and 54** are objected because of the following informalities:

Claim 25 recites "...2a)...providing a second query distribution scheme by dividing each query sequence into n+1 query sequence segment..." and "...2b) for each of the n+1 query sequences under the second query distribution scheme, constructing a first query group and a second query group according to the first query distribution scheme by placing individual query sequence segments in one of said query groups..." which is unclear and confusing.

Step 1a and 1c teach using "first query distribution scheme" to divide each query sequence into query sequence segments and form two query groups. Step 2a and 2b teach using "second query distribution scheme" to divide each query sequence into query sequence segments, but still use "first query distribution scheme..." According to the specification, Step 2c and 2d should use "second query distribution scheme" to form query groups.

Appropriate correction/clarification is required.

Claim 54 recites "A computer program..." It should be changed to –A computer product--.

Appropriate correction is required.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

5. **Claims 25, 31-34, 36, 38-41, 43-50, 52-54 and 56 rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson).**

For claim 25, Califano discloses a computer implemented method of searching biochemical sequence information for a plurality of query sequences in a set of target sequence fragments, allowing for mismatches at up to n sequence positions, comprising:

1a) providing a first query distribution scheme by dividing each query sequence into n+1 query sequence segments (Califano: column 5, lines 40-45, "the reference sequence is partitioned into substrings of contiguous tokens 35 at least two of which are non contiguously appended together 40 to form reference tuples.", where "segment" is read on "token") **and providing a corresponding first target distribution scheme by dividing each target fragment into at least n+1 target sequence fragment segments** (Califano: column 5, lines 32-35, "selecting an original string 10 from a database. The string is then partitioned into substrings of contiguous tokens 15 at least two of which are non contiguously appended together to form original tuples 20.");

1b) for each of the n+1 query sequences under the first target distribution scheme, constructing a first query group and a second query group according to the first query distribution scheme by placing individual query sequence

segments in one of said query group so that at least n query sequence segments are contained in the second query group (Califano: column 5, lines 32-35, "the reference sequence is partitioned into substrings of contiguous tokens 35 at least two of which are non contiguously appended together 40 to form reference tuples.");

1c) for each of the target sequence fragment segments under the first target distribution scheme, constructing a first target group and a second target group according to the first target distribution scheme by placing individual target sequence fragment segments in one of said target groups,(Califano: column 1, lines 35-40, "All tokens in the two sequences to be compared are considered pairwise to compute all possible candidate alignments between the two sequences.", column 8, lines 12-15, "Taking all possible ordered combinations of 3 contiguous and non contiguous substrings from this set of 17 substrings, it is possible to create 680 3 - tuples." column 5, lines 32-35, "selecting an original string 10 from a database. The string is then partitioned into substrings of contiguous tokens 15 at least two of which are non contiguously appended together to form original tuples 20.");

1d) for each of the n+1 query sequences, comparing the first query group with the corresponding first target group to identify a potential matches under the first query distribution scheme and the corresponding first target distribution scheme (Califano: column 1, lines 35-40, "All tokens in the two sequences

to be compared are considered pairwise to compute all possible candidate alignments between the two sequences.", column 8, lines 12-15, "Taking all possible ordered combinations of 3 contiguous and non contiguous substrings from this set of 17 substrings, it is possible to create 680 3 - tuples."column 5, lines 46-47, "The reference indexes are then compared to the original indexes 50.").

4) comparing the second query group with the second target group to identify a match, thereby identifying a query sequence in the set of target sequence fragments, while allowing for mismatches in up to n sequence positions (Colifano: column 2, lines 1-16, "The BLAST technique does an in-depth comparison of the original and reference sequence only if they satisfy an initial minimal similarity test which can be performed very quickly. This is done by heuristically determining whether the length of the MSP (maximal segment pair) is above a given threshold. *The MSP is the pair of identical length substrings of the reference string and sequence string that has the best score for mutations. If this test is successful a more complete and costly similarity analysis is performed using FASTP-FASTA type algorithms.* This reduces the amount of computation at risk of missing some matches that do not satisfy the initial criteria. About 20% of the similarities detected with the Needleman-Wunch algorithm are not picked up by

BLAST. Also the approach remains inherently sequential since some computation must be performed for each token in the set of original strings." column 4, lines 55-63, "information in the EIT is used to locate token sequences on an original string in the database which correspond (exactly or similarly) to the reference sequence of tokens…", column 5, lines 32-35, where "group" is read on "tuple", and "tuples" indicates there are many group (e.g. first group, second group...etc.).

However, Califano does not explicitly disclose

2a) providing a second query distribution scheme by dividing each query sequence into n+1 query sequence segments and providing a corresponding second target distribution scheme by dividing each target fragment into at least n+1 target sequence fragment segments;

2b) for each of the n+1 query sequences under the second query distribution scheme, constructing a first query group and a second query group according to the first query distribution scheme by placing individual query sequence segments in one of said query groups so that at least n query sequence segments are contained in the second query group;

2c) for each of the target sequence fragment segments under the second target distribution scheme, constructing a first target group and a second target group

according to the first target distribution scheme by placing individual target sequence fragment segments in one of said query groups;

2d) for each of the n+1 query sequences, comparing the first query group for a sequence identical with the corresponding first target group to identify a potential matches under the second query distribution scheme and the corresponding second target distribution scheme; and

3) optionally repeating steps 2a) to 2d) for further query distribution schemes and corresponding target distribution schemes;

wherein for each of the potential matches identified under the first distribution schemes obtained in steps 1 d), under the second distribution schemes obtained in step 2d), and in the distribution schemes in step 3), subsequently; while allowing for mismatches in up to n sequence positions

Bjornson discloses 2a) providing a second query distribution scheme by dividing each query sequence into n+1 query sequence segments and providing a corresponding second target distribution scheme by dividing each target fragment into at least n+1 target sequence fragment segments (Bjornson: column 3, line 55-column 4, line 10, "…for searching a plurality of query sequences against at least one sequence database containing a plurality of sequence records. The method comprises the steps of: a. partitioning the plurality of query sequences into a set of smaller subsets of query sequences; b. partitioning the at least one sequence database into a set of smaller subdatabases…");

2b) for each of the n+1 query sequences under the second query distribution scheme, constructing a first query group and a second query group according to the first query distribution scheme by placing individual query sequence segments in one of said query groups so that at least n query sequence segments are contained in the second query group; 2c) for each of the target sequence fragment segments under the second target distribution scheme, constructing a first target group and a second target group according to the first target distribution scheme by placing individual target sequence fragment segments in one of said query groups (Bjornson: column 3, line 55-column 4, line 10, "…c. designating searching tasks to be performed by associating each of said subsets of query sequences with one or more of said subdatabases, assigning each searching task to one of a group of computers operating in parallel, wherein each member of the group of computers operating in parallel has at least one searching task assigned thereto, and executing at least some of the assigned searching tasks using the group of computers operating in parallel…");

2d) for each of the n+1 query sequences, comparing the first query group for a sequence identical with the corresponding first target group to identify a potential matches under the second query distribution scheme and the corresponding second target distribution scheme (Bjornson: column 3, line 55-column 4, line 10, "…and d. collecting search results from the

executed searching tasks and generating a unified sequence search result in accordance with the collected search results.”); **and**

3) optionally repeating steps 2a) to 2d) for further query distribution schemes and corresponding target distribution schemes; wherein for each of the potential matches identified under the first distribution schemes obtained in steps 1d), under the second distribution schemes obtained in step 2d), and in the distribution schemes in step 3), subsequently (Bjornson: column 3, line 55-column 4, line 10, “The invention relates to a computer-implemented method and apparatus for searching a plurality of query sequences against at least one sequence database containing a plurality of sequence records. The method comprises the steps of: a. partitioning the plurality of query sequences into a set of smaller subsets of query sequences; b. partitioning the at least one sequence database into a set of smaller subdatabases; c. designating searching tasks to be performed by associating each of said subsets of query sequences with one or more of said subdatabases, assigning each searching task to one of a group of computers operating in parallel, wherein each member of the group of computers operating in parallel has at least one searching task assigned thereto, and executing at least some of the assigned searching tasks using the group of computers

operating in parallel; and d. collecting search results from the executed searching tasks and generating a unified sequence search result in accordance with the collected search results.")

while allowing for mismatches at up to n sequence positions (Bjornson: column 2, lines 26-32, "first identify segments, with or without gaps, that are similar in a query sequence and a database sequence, then to evaluate the statistical significance of all such matches that are identified, and finally to summarize only those matches that satisfy a preselected threshold of significance.", column 6, lines 14-32, "...such that the locally optimal ungapped alignment between the two members of said HSP achieves a score at least equal to a specified integer minimum score value or an e-score lower than a specified e-score threshold...").

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Method and apparatus for high-performance sequence comparison" as taught by Bjornson, because it would provide Califano's method with the enhanced capability of "comparing sequences for similarity " (Bjornson: column 6, lines 6-7).

For claim 31, Califano and Bjornson disclose the modified computer implemented method of claim 25, further comprising:

for each distinct distribution of query sequence segments, constructing a first query table indexed by possible values of the first query groups, wherein the entries in the first query table provide access to each second query group by using as an index the value of a corresponding first query group (Colifano: column 3, lines 21-29, "A large number of *indexes* are generated for each original string and are used to store a information record referring to the original string in a *look-up table*. During recognition, a large number of indexes are formed from a reference string. These are used to recover the information in the look-up table and to accumulate evidence for one or more original strings.").

For claim 32, Califano and Bjornson disclose the modified computer implemented method of claim 31, further comprising:

for each distinct distribution of query sequence segments, constructing a second query table providing access to each second query group, wherein the entries in the first query table provide references to appropriate entries in the second query table (Colifano: column 3, lines 21-29, lines 46-47, column 4, lines 27-63).

For claim 33, Califanoa and Bjornson disclose the modified computer implemented method of claim 31, further comprising:

for each first target group constructed in step 1c) or 2c), implementing step 1d) or 2d) by using each first target group to form an index into the first query table (Colifano: column 3, lines 21-29, lines 46-47).

For claim 34, Califano and Bjornson disclose the modified computer implemented method of claim 31, wherein, that the first query group of a first distribution is the same as the second query group of a second distribution, respective first query tables for each of the two distinct distributions are at least one of constructed and used concurrently (Colifano: column 3, lines 21-29, column 8, lines 12-15)

distributions of query sequence segments (Bjornson: column 4, 51-59)**.**

For claim 36, Califano and Bjornson disclose the modified computer implemented method of claim 25, wherein each query sequence of the plurality of query sequences and the target sequence fragments comprise nucleotide sequence data (Califano: column 1, lines 25-30, column 2, lines 62-67)**.**

For claim 38, Califano and Bjornson disclose the modified computer implemented method of claim 25, wherein n is at least two (Califano: column 6, lines 60-61)**.**

For claim 39, Califano and Bjornson disclose the modified computer implemented method of claim 25, wherein each query sequence of the plurality of query sequences and the target sequence fragments are divided into an even number of query sequence segments and target sequence fragment segments, and further wherein the query sequence segments and the target sequence

fragment segments are distributed in equal numbers between the first query group and the second query group and the first target group and a second target group (Bjornson: column 11, lines 7-10).

For claim 40, Califano and Bjornson disclose the modified computer implemented method of claim 25, wherein the n+1 query sequence segments are formed from a splitting of each query sequence of the plurality of query sequences (Califano: column 5, lines 32-35),

For claim 41, Califano and Bjornson discloses the modified computer implemented method of claim 25, wherein the n+1 query sequence segments are formed from a coding or scrambling of each query sequence of the plurality of query sequences (Califano: column 1, lines 35-40, column 8, lines 12-15).

For claim 43, Califano and Bjornson disclose the modified computer implemented method claim 25, further comprising: constructing or computing at least one hash function table (Califano: column 2, lines 52-55).

Claim 44 is rejected as substantially similar as claims 25, for the similar reasons.

Claim 45 is rejected as substantially similar as claims 27, for the similar reasons.

Claim 46 is rejected as substantially similar as claims 28, for the similar reasons.

Claim 47 is rejected as substantially similar as claims 31, for the similar reasons.

Claim 48 is rejected as substantially similar as claims 32, for the similar reasons.

Claim 49 is rejected as substantially similar as claims 40, for the similar reasons.

Claim 50 is rejected as substantially similar as claims 41, for the similar reasons.

Claim 52 is rejected as substantially similar as claims 43, for the similar reasons.

For claim 53, Califano and Bjornson disclose the modified apparatus of claim 44, wherein the apparatus is a personal computer or a desk top computer (Califano: column 5, lines 26-29)**.**

Claim 54 is rejected as substantially similar as claims 25, for the similar reasons.

For claim 56, Califano and Bjornson disclose the modified computer program of claim 54, wherein the computer program is loadable on a device for searching, over a network connection. 9 (Bojornson: column 5, lines 49-65).

6. **Claims 29, 30 and 37 are rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson) as applied in claim 25 above, and further in view of Patzer (U.S. Patent No.: US 2004/0059721 A1).**

For claim 29, Califano and Bjornson disclose the modified computer implemented method of claim 25.

However, Califano and Bjornson do not explicitly disclose wherein step 4) is carried out by applying an exclusive OR operation to a binary representation of each of the second query group and the second target group.

Patzer discloses wherein step 4) is carried out by applying an exclusive OR operation to a binary representation of each of the second query group and the second target group (Patzer: page 1, paragraph [0012], "Using this encoding, the system adds the result of every *XOR* nucleotide comparison")**.**

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano

by implementing "Method and apparatus for high-performance sequence comparison" as taught by Patzer, because it would provide Califano and Bjornson's modified method with the enhanced capability of "in order to obtain a sum score quantifying the dissimilarity of a particular sequence alignment." (Patzer: page 1, paragraph [0012]).

For claim 30, Califano, Bjornson and Patzer disclose the modified computer implemented method of claim 29, wherein a result is analyzed using a lookup table (Califano: column 1, lines 45-59, "...are matched for both sequences using a look-up table that is created from the reference string. The score for each candidate match is computed and the best score is selected...").

the exclusive OR operation (Patzer: page 1, paragraph [0012]).

For claim 37, Califano and Bjornson disclose the modified computer implemented method of claim 36.

However, Califano and Bjornson do not explicitly disclose wherein each query sequence of the plurality of query sequences and the target sequence fragments are binary encoded.

Patzer discloses wherein each query sequence of the plurality of query sequences and the target sequence fragments are binary encoded (Patzer: page 5, paragraph [0096]).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token

sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Method and apparatus for high-performance sequence comparison" as taught by Patzer, because it would provide Califano and Bjornson's modified method with the enhanced capability of "in order to obtain a sum score quantifying the dissimilarity of a particular sequence alignment." (Patzer: page 1, paragraph [0012]).

7. **Claims 35 and 55 are rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson) as applied in claims 25 and 54 above, and further in view of Walker et al. (U.S. Patent No.: US 6,633,817 B1, hereinafter, Walker).**

For claim 35, Califano and Bjornson disclose the modified computer implemented method of claim 25.

However Califano and Bjornson do not explicitly disclose wherein target sequence fragments in the set of target sequence fragments comprise overlapping fragments of one or more target sequences.

Walker discloses wherein target sequence fragments in the set of target sequence fragments comprise overlapping fragments of one or more target sequences (Walker: column 1, lines 61-65, "`partitioned into a plurality of overlapping windows or fragments...`")**.**

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "`Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings`" as taught by Califano by implementing "`Sequence database search with sequence search trees`" as taught by Walker, because it would provide Califano and Bjornson's modified method with the enhanced capability of "`organizing and searching database`

sequences that is fast and efficient, and at the same time provides a high degree of accuracy, that is, one that identifies sequences similar to a query sequence." (Walker: column 1, lines 46-50).

For claim 55, Califano and Bjornson disclose the modified computer program of claim 54.

However, Califano and Bjornson do not explicitly disclsoe wherein the computer program is stored on a removable computer-readable storage medium.

Walker discloses the computer program of claim 54, wherein the computer program is stored on a removable computer-readable storage medium (Walker: claim 22).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Sequence database search with sequence search trees" as taught by Walker, because it would provide Califano and Bjornson's modified program with the enhanced capability of storing and executing a program by computers.

8. **Claims 42 and 51 are rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson)**

as applied in claims 25 and 54 above, and further in view of Myers et al. (U.S. Patent No.: US 6,714,874 B1, hereinafter, Myers).

For claim 42, Califano and Bjornson discloses the modified computer implemented method of claim 25, further comprising: using a hash function to split each query sequence of the plurality of query sequences and the target sequence fragments (Califano: column 2, lines 52-55)**.**

However, Califano and Bjornson do not explicitly disclose further comprising: using a hash function to split each query sequence of the plurality of query sequences and the target sequence fragments into prefixes and suffixes.

Myers discloses further comprising: using a hash function to split each query sequence of the plurality of query sequences and the target sequence fragments into prefixes and suffixes (Myers: column 9, lines 52-53, column 13, 52-61)**.**

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Method and system for the assembly of a whole genome using a shot-gun data set" as taught by Myers, because it would provide Califano and Bjornson's modified method with the enhanced capability of "A containment relationship between fragment-ends is a further

refinement of a containment relationship between fragments."

(Myers: column 13, lines 50-52).

Claim 51 is rejected as substantially similar as claims 42, for the similar reasons.

9. **Claim 57 is rejected under 35 U.S.C. 103(a) as being unpatentable over Califano et al. (U.S. Patent No.: US 5,577,249 B1, hereinafter, Califano), in view of Bjornson et al. (U.S. Patent No.: US 6,691,109 B2, hereinafter, Bjornson) as applied in claim 25 above, and further in view of Harris et al. (U.S. Pub. No.: US 2002/0022243 A1, hereinafter, Harris).**

For claim 57, Califano and Bjornson disclose the modified computer implemented method of claim 25.

However, Califano and Bjornson does not explicitly disclose, wherein each query sequence of the plurality of query sequences and the target sequence fragments comprise polypeptide sequence data.

Harris discloses wherein each query sequence of the plurality of query sequences and the target sequence fragments comprise polypeptide sequence data. (Harris: page 11, paragraph [0141]).

It would have been obvious to one of ordinary skill in the art at the time the invention was made to improve upon "Method for finding a reference token sequence in an original token string within a database of token strings using appended non-contiguous substrings" as taught by Califano by implementing "Profiling of protease specificity using

combinatorial fluorogenic substrate libraries" as taught by Harris, because it would provide Califano and Bjornson's modified method with the enhanced capability of "provides a computer system for comparing a query polypeptide sequence or query peptide sequence specificity to a database containing an array of data structures..." (Harris: page 11, paragraph [0141]).

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to YU ZHAO whose telephone number is (571)270-3427. The examiner can normally be reached on Monday-Friday 7:30am-5:00pm EST.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Tony Mahmoudi can be reached on (571) 272-4078. The fax phone number for the organization where this application or proceeding is assigned is 571-270-4427.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Date: 10/21/2010

/Yu Zhao/

Examiner, Art Unit 2169

/Tony Mahmoudi/

Supervisory Patent Examiner, Art Unit 2169